IN THE SPECIFICATION:

Please replace the title of the application as shown beginning on page 1, line 3, with the following new title:

METHOD OF IDENTIFYING A COMPOUND THAT MODULATES A BIOLOGICAL ACTIVITY OF AN HERG/KCR1 COMPLEX

Please replace the paragraph beginning at page 9, line 23, with the following rewritten paragraph:

Brief Description of the Drawings

Figure 1A is an alignment depicting the alignment of deduced amino acid sequences of the rat and human KCR1 (SEQ ID NOs: 9 and 2, respectively), with identical amino acids in the human sequence identified by the dashes. Putative transmembrane segments (TMD 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 and 12) were identified by hydropathy analysis.

Please replace the paragraph beginning at page 23, line 14, with the following rewritten paragraph:

The list of drugs that block HERG is extremely long, and more are identified almost daily. A web site that contains a partial list is: http://www.ihc.com/research/longqt.html. Representative drugs include but are not limited to: anesthetics/asthma medications (e.g. epinephrine), antihistamines (e.g. terfenadine, astemizole, and diphenhydramine), antibiotics (e.g. erythromycin, trimethoprim, and sulfamethoxazole pentamidine), heart medications (e.g. quinidine, procainamide, disopyramide, sotalol, probucol, bepridil), gastrointestinal medications (e.g. cisapride), antifungal drugs (e.g. ketoconazole, fluconazole, and itraconazole), psychotropic drugs (e.g. amitriptyline (tricyclics), phenothiazine derivatives, haloperidol, risperidone, and pimozide), and diuretics (e.g. indapamide). These representative drugs, as well as others, are implicate in acquired Long QT Syndrome.

Please replace the paragraph beginning at page 42, line 8, with the following rewritten paragraph:

Between mammalian species, e.g., human and mouse, homologs have substantial sequence similarity, i.e. at least 75% sequence identity between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which can be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, etc. A reference sequence will usually be at least about 18 nt long, more usually at least about 30 nt long, and can extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., (1990) *J. Mol. Biol.* 215: 403-10. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength W = 11, an expectation E = 10, a cutoff of 100, M = 5, N = -4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix. See Henikoff & Henikoff, (1989) Proc Natl Acad Sci U.S.A. 89: 10915.

Please replace the reference found at page 106, line 24, with the following reference:

~~http://www.~~ihc.com/research/longqt.html